STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/578, 493_
Source: _IFWP_
Date Processed by STIC: _05/17/2006_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/578,493_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. **If intentional,** please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11____Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa

"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

IFWP

RAW SEQUENCE LISTING   DATE: 05/17/2006
PATENT APPLICATION: US/10/578,493   TIME: 10:01:13

Input Set : A:\67987.000002.ST25.txt
Output Set: N:\CRF4\05172006\J578493.raw

```
      3 <110> APPLICANT: Desire, Laurent
      5 <120> TITLE OF INVENTION: BACE455, AN ALTERNATIVE SPLICE VARIANT OF THE HUMAN
      6       BETA-SECRETASE
      8 <130> FILE REFERENCE: 67987.000002
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/578,493
C--> 11 <141> CURRENT FILING DATE: 2006-05-05
     13 <160> NUMBER OF SEQ ID NOS: 33
     15 <170> SOFTWARE: PatentIn version 3.3
     17 <210> SEQ ID NO: 1
     18 <211> LENGTH: 1368
     19 <212> TYPE: DNA
     20 <213> ORGANISM: Homo sapiens
     22 <400> SEQUENCE: 1
     23 atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgct gcctgcccac      60
     25 ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc ccccctgggg     120
     27 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt     180
     29 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc     240
     31 gtgggcagcc ccccgcagac gctcaacatc ctggtggata caggcagcag taactttgca     300
     33 gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca     360
     35 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag     420
     37 ctgggcaccg acctggtaag catcccccat ggccccaacg tcactgtgcg tgccaacatt     480
     39 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg     540
     41 gggctggcct atgctgagat tgccaggatc attggaggta tcgaccactc gctgtacaca     600
     43 ggcagtctct ggtatacacc catccggcgg gagtggtatt atgaggtcat cattgtgcgg     660
     45 gtggagatca atggacagga tctgaaaatg gactgcaagg agtacaacta tgacaagagc     720
     47 attgtggaca gtggcaccac caaccttcgt ttgcccaaga aagtgtttga agctgcagtc     780
     49 aaatccatca aggcagcctc ctccacggag aagttccctg atggtttctg gctaggagag     840
     51 cagctggtgt gctggcaagc aggcaccacc ccttggaaca ttttcccagt catctcactc     900
     53 tacctaatgg gtgaggttac caaccagtcc ttccgcatca ccatccttcc gcagcaatac     960
     55 ctgcggccag tggaagatgt ggccacgtcc caagacgact gttacaagtt tgccatctca    1020
     57 cagtcatcca cgggcactgt tatgggagct gttatcatgg agggcttcta cgttgtcttt    1080
     59 gatcgggccc gaaaacgaat tggctttgct gtcagcgctt gccatgtgca cgatgagttc    1140
     61 aggacggcag cggtggaagg ccctttttgtc accttggaca tggaagactg tggctacaac    1200
     63 attccacaga cagatgagtc aaccctcatg accatagcct atgtcatggc tgccatctgc    1260
     65 gccctcttca tgctgccact ctgcctcatg gtgtgtcagt ggcgctgcct ccgctgcctg    1320
     67 cgccagcagc atgatgactt tgctgatgac atctccctgc tgaagtga                 1368
     70 <210> SEQ ID NO: 2
     71 <211> LENGTH: 455
     72 <212> TYPE: PRT
     73 <213> ORGANISM: Homo sapiens
     75 <400> SEQUENCE: 2
     77 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
     78 1               5                   10                  15
```

file://C:\CRF4\Outhold\VsrJ578493.htm   5/17/2006

```
 81 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 82          20              25              30
 85 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 86          35              40              45
 89 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 90      50              55              60
 93 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 94 65              70              75              80
 97 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 98              85              90              95
101 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
102          100             105             110
105 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
106          115             120             125
109 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
110      130             135             140
113 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
114 145             150             155             160
117 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
118          165             170             175
121 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Ile Ile Gly
122          180             185             190
125 Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
126          195             200             205
129 Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
130      210             215             220
133 Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
134 225             230             235             240
137 Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
138          245             250             255
141 Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
142          260             265             270
145 Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
146          275             280             285
149 Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
150      290             295             300
153 Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
154 305             310             315             320
157 Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
158          325             330             335
161 Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
162          340             345             350
165 Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
166          355             360             365
169 Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
170      370             375             380
173 Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
174 385             390             395             400
177 Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
```

RAW SEQUENCE LISTING   DATE: 05/17/2006
PATENT APPLICATION: US/10/578,493   TIME: 10:01:13

Input Set : A:\67987.000002.ST25.txt
Output Set: N:\CRF4\05172006\J578493.raw

```
178                 405              410              415
181 Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
182             420              425              430
185 Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala
186         435              440              445
189 Asp Asp Ile Ser Leu Leu Lys
190     450              455
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 6
195 <212> TYPE: PRT
196 <213> ORGANISM: artificial
198 <220> FEATURE:
199 <223> OTHER INFORMATION: distinctive fragment
201 <400> SEQUENCE: 3
203 Ile Ala Arg Ile Ile Gly
204 1           5
207 <210> SEQ ID NO: 4
208 <211> LENGTH: 7
209 <212> TYPE: PRT
210 <213> ORGANISM: artificial
212 <220> FEATURE:
213 <223> OTHER INFORMATION: distinctive fragment
215 <400> SEQUENCE: 4
217 Glu Ile Ala Arg Ile Ile Gly
218 1           5
221 <210> SEQ ID NO: 5
222 <211> LENGTH: 8
223 <212> TYPE: PRT
224 <213> ORGANISM: artificial
226 <220> FEATURE:
227 <223> OTHER INFORMATION: distinctive fragment
229 <400> SEQUENCE: 5
231 Glu Ile Ala Arg Ile Ile Gly Gly
232 1           5
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 8
237 <212> TYPE: PRT
238 <213> ORGANISM: artificial
240 <220> FEATURE:
241 <223> OTHER INFORMATION: distinctive fragment
243 <400> SEQUENCE: 6
245 Ala Glu Ile Ala Arg Ile Ile Gly
246 1           5
249 <210> SEQ ID NO: 7
250 <211> LENGTH: 9
251 <212> TYPE: PRT
252 <213> ORGANISM: artificial
254 <220> FEATURE:
255 <223> OTHER INFORMATION: AEIARIIGG
```

[handwritten annotation]: Insufficient Explanation. what is the Source of genetic Material. Pls see Item 11 on Error Summary Sheet.

RAW SEQUENCE LISTING   DATE: 05/17/2006
PATENT APPLICATION: US/10/578,493   TIME: 10:01:13

Input Set : A:\67987.000002.ST25.txt
Output Set: N:\CRF4\05172006\J578493.raw

```
257 <400> SEQUENCE: 7
259 Ala Glu Ile Ala Arg Ile Ile Gly Gly
260 1               5
263 <210> SEQ ID NO: 8
264 <211> LENGTH: 10
265 <212> TYPE: PRT
266 <213> ORGANISM: artificial
268 <220> FEATURE:
269 <223> OTHER INFORMATION: distinctive fragment
271 <400> SEQUENCE: 8
273 Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
274 1               5                   10
277 <210> SEQ ID NO: 9
278 <211> LENGTH: 9
279 <212> TYPE: PRT
280 <213> ORGANISM: artificial
282 <220> FEATURE:
283 <223> OTHER INFORMATION: distinctive fragment
285 <400> SEQUENCE: 9
287 Tyr Ala Glu Ile Ala Arg Ile Ile Gly
288 1               5
291 <210> SEQ ID NO: 10
292 <211> LENGTH: 10
293 <212> TYPE: PRT
294 <213> ORGANISM: artificial
296 <220> FEATURE:
297 <223> OTHER INFORMATION: distinctive fragment
299 <400> SEQUENCE: 10
301 Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly
302 1               5                   10
305 <210> SEQ ID NO: 11
306 <211> LENGTH: 11
307 <212> TYPE: PRT
308 <213> ORGANISM: artificial
310 <220> FEATURE:
311 <223> OTHER INFORMATION: distinctive fragment
313 <400> SEQUENCE: 11
315 Tyr Ala Glu Ile Ala Arg Ile Ile Gly Gly Ile
316 1               5                   10
319 <210> SEQ ID NO: 12
320 <211> LENGTH: 18
321 <212> TYPE: DNA
322 <213> ORGANISM: artificial
324 <220> FEATURE:
325 <223> OTHER INFORMATION: probe
327 <400> SEQUENCE: 12
328 attgccagga tcattgga                                    18
331 <210> SEQ ID NO: 13
332 <211> LENGTH: 10
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[handwritten annotation: "Same error"]

RAW SEQUENCE LISTING   DATE: 05/17/2006
PATENT APPLICATION: US/10/578,493 TIME: 10:01:13

Input Set : **A:\67987.000002.ST25.txt**
Output Set: **N:\CRF4\05172006\J578493.raw**

```
333 <212> TYPE: DNA
334 <213> ORGANISM: artificial
336 <220> FEATURE:
337 <223> OTHER INFORMATION: primer
339 <400> SEQUENCE: 13
340 aggcatcctg                                              10
343 <210> SEQ ID NO: 14
344 <211> LENGTH: 10
345 <212> TYPE: DNA
346 <213> ORGANISM: artificial
348 <220> FEATURE:
349 <223> OTHER INFORMATION: primer
351 <400> SEQUENCE: 14
352 gggctggcct                                              10
355 <210> SEQ ID NO: 15
356 <211> LENGTH: 10
357 <212> TYPE: DNA
358 <213> ORGANISM: artificial
360 <220> FEATURE:
361 <223> OTHER INFORMATION: primer
363 <400> SEQUENCE: 15
364 atgctgagat                                              10
367 <210> SEQ ID NO: 16
368 <211> LENGTH: 6
369 <212> TYPE: DNA
370 <213> ORGANISM: artificial
372 <220> FEATURE:
373 <223> OTHER INFORMATION: primer
375 <400> SEQUENCE: 16
376 tgccag                                                   6
379 <210> SEQ ID NO: 17
380 <211> LENGTH: 6
381 <212> TYPE: DNA
382 <213> ORGANISM: artificial
384 <220> FEATURE:
385 <223> OTHER INFORMATION: primer
387 <400> SEQUENCE: 17
388 gatcat                                                   6
391 <210> SEQ ID NO: 18
392 <211> LENGTH: 10
393 <212> TYPE: DNA
394 <213> ORGANISM: artificial
396 <220> FEATURE:
397 <223> OTHER INFORMATION: primer
399 <400> SEQUENCE: 18
400 tggaggtatc                                              10
403 <210> SEQ ID NO: 19
404 <211> LENGTH: 10
405 <212> TYPE: DNA
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/17/2006
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Input Set : **A:\67987.000002.ST25.txt**
Output Set: **N:\CRF4\05172006\J578493.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 5

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29
Seq#:30,31,32,33

VERIFICATION SUMMARY   DATE: 05/17/2006
PATENT APPLICATION: US/10/578,493   TIME: 10:01:14

Input Set : **A:\67987.000002.ST25.txt**
Output Set: **N:\CRF4\05172006\J578493.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0